

20 25 30

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu  
35 40

<210> 32  
<211> 262  
<212> DNA  
<213> Homo sapiens

<220>  
<223> Intron X. Complete length unknown

<400> 32  
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gggtgccagg tgccctgcaa gtagaggggc tctcagaggc gtctggotgg catgggtgga 120  
cgtggccccg ggcattggcct tctgcgtgtg ctgcccgtgg tgccctgagc cctcactgag 180  
tcggtggggg cttgtggctt cccgtgagct tccccctagt ctgttgtctg gctgagcaag 240  
cctcctgagg ggctctctat tg 262

<210> 33  
<211> 218  
<212> DNA  
<213> Homo sapiens

<220>  
<223> Partial Sequence of Genomic Intron (approximately 2.7 kb)

<400> 33  
gtggctgtgc tttgggttaa cttccttttt aaccagaagt gcgtttgagc cccacatttg 60  
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cggcgccac ccatttgtgc gcacagttag gtggccgagg tgccggtgcc tccagaaaag 180  
cagcgtgggg gtgtaggggg agctcctggg gcaggggac 218

<210> 34  
<211> 2031  
<212> DNA  
<213> Homo sapiens

<220>  
<221> modified\_base  
<222> (1767)..(1769)  
<223> Wherein N is A, C, G or T

<220>  
<223> Truncated Telomerase

<400> 34  
atgccgcgcg ctccccgctg ccgagccgtg cgtccctgc tggcagcca ctaccgcgag 60  
gtgctgcgcg tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120  
cgccgggaac cggcggcctt ccgcgcgctg gtggcccagt gcctggtgtg cgtgcccttg 180  
gacgcacggc cgcctccctc cgcctccctc ttccgcagg tgctctgctt gaaggagctg 240  
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ttcgogctgc tggacggggc ccgcgggggg ccccccagg ccttcaccac cagcgtgcgc 360  
agctacctgc ccaacacggt gaccgacgca ctgcggggga ggggggcgtg ggggctgctg 420  
ctgcgcgcgc tgggcgacga cgtgctggtt cactgctgg caogctgcgc gctctttgtg 480

Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly  
1045 1050 1055

Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe  
1060 1065 1070

Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu  
1075 1080

<210> 51

<211> 2135

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1871)..(1873)

<223> Wherein N is A, C, G or T

<220>

<223> Truncated Telomerase (ver. 2); with  
Intron Y

<400> 51

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atgccgcgcg ctccccgctg ccgagccgtg cgtccctgc tggcagcca ctaccgcgag 60
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cgcgggggacc cggcggtctt ccgcgcgctg gtggcccaag gctgggtgtg cgtgcccgtg 180
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gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggg gcttcccccg cagggtgctc gcctgaagga gctgggtggc cgagtgtgtc 360
agaggctgtg cgagcggcgc gegaagaacg tgctggcctt cggcttgcg ctgctggacg 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaca 480
cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgtgc cgcgtggcg 540
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ccacgttcca aaagaacagg ctctttttct accggaagag tgtctggagc aagtggaaa 1860
gcattggaat nnnagacgtc accagggggg ttgaccgcg gactggcgct cccagggtt 1920
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gactatagga ccaggtgtcc aggtgccctg caagtagagg ggctctcaga ggogtctggc 1980  
 tggcatgggt ggacgtggcc ccgggcatgg cettctgcgt gtgctgacgt gggtagccctg 2040  
 agccctcact gagtcgggtg gggcttgggg cttcccgatg gcttcccccct agtctgttgt 2100  
 ctggctgagc aagcctcctg aggggctctc tattg 2135

<210> 52

<211> 622

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Telomerase (ver.2); encoded  
 by SEQ ID NO:51 and ORF1 of Intron Y

<400> 52

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
 1 5 10 15  
 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly  
 65 70 75 80  
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu  
 85 90 95  
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys  
 100 105 110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
 115 120 125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
 130 135 140  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
 145 150 155 160  
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
 165 170 175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
 180 185 190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
 195 200 205  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
 210 215 220  
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser

225	23	235	240
Val Arg Glu Ala Gly	Val Pro Leu Gly Leu	Pro Ala Pro Gly Ala Arg	
245	250	255	
Arg Arg Gly Gly Ser Ala Ser Arg	Ser Leu Pro Leu Pro Lys Arg Pro		
260	265	270	
Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly			
275	280	285	
Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe			
290	295	300	
Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu			
305	310	315	320
Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln			
325	330	335	
His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp			
340	345	350	
Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser			
355	360	365	
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu			370
375	380		
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu			
385	390	395	400
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu			
405	410	415	
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly			
420	425	430	
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro			
435	440	445	
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys			
450	455	460	
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg			
465	470	475	480
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr			
485	490	495	
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp			
500	505	510	
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe			
515	520	525	
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp			
530	535	540	

Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly  
 610 615 620

<210> 53  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Splicing Variant of Human Telomerase encoded by  
 Intron Y, ORF2, before the termination codon.  
 SEQ ID NOs: 51,55,59,63,67,71,75,79,83 encode this  
 fragment

<400> 53  
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
 1 5 10 15  
 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ala Ser Pro Gly Ser Ala  
 65 70 75 80  
 Ser Gly Trp Gly

<210> 54  
 <211> 537  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Telomerase (var. 2); encoded  
 by SEQ ID NO:51, with Y intron, ORF2, after the  
 termination codon

<210> 154  
 <211> 4  
 <212> PRT  
 <213> Homo sapiens

<400> 154  
 Arg Ala Thr Ser  
 1

<210> 155  
 <211> 622  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Telomerase (ver.2); encoded  
 by SEQ ID NO:51, with Y Intron ORF3

<400> 155  
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
 1 5 10 15  
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg  
 65 70 75 80  
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu  
 85 90 95  
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys  
 100 105 110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
 115 120 125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
 130 135 140  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
 145 150 155 160  
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
 165 170 175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
 180 185 190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro

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